SEQUENCE LISTING

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Jang, Jihoon
Yum, Jungsun
Chung, Soo-il

<120> Novel Detoxified Mutants of Escherichia coli Heat-Labile Enterotoxin

<130> 58049-00003

<140> US 10/088,202
<141> 2002-03-15

<150> PCT/KR99/00555
<151> 1999-09-15

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<170> PatentIn version 3.5

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<212> DNA
<213> Artificial sequence

<220>
<223> Primer

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<221> primer_bind
<222> (1)..(52)

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Tyr Ala Asn Gly Asp Arg Leu Tyr Arg Ala Asp Ser Arg Pro Pro Asp
            20                  25                  30

Glu Ile Lys Arg Ser Gly Gly Leu Met Pro Arg Gly His Asn Glu Tyr
        35                  40                  45

Phe Asp Arg Gly Thr Gln Met Asn Ile Asn Leu Tyr Asp His Ala Arg
    50                  55                  60

Gly Thr Gln Thr Gly Phe Val Arg Tyr Asp Asp Gly Tyr Val Ser Thr
65                  70                  75                  80

Tyr Leu Ser Leu Arg Ser Ala His Leu Ala Gly Gln Ser Ile Leu Ser
                85                  90                  95

Gly Tyr Ser Thr Tyr Tyr Ile Tyr Val Ile Ala Thr Ala Pro Asn Met
            100                 105                 110

Phe Asn Val Asn Asp Val Leu Gly Val Tyr Ser Pro His Pro Tyr Glu
        115                 120                 125

Gln Glu Val Ser Ala Leu Gly Gly Ile Pro Tyr Ser Gln Ile Tyr Gly
    130                 135                 140

Trp Tyr Arg Val Asn Phe Gly Val Ile Asp Glu Arg Leu His Arg Asn
145                 150                 155                 160

Arg Glu Tyr Arg Asp Arg Tyr Tyr Arg Asn Leu Asn Ile Ala Pro Ala
                165                 170                 175

Glu Asp Gly Tyr Arg Leu Ala Gly Phe Pro Pro Asp His Gln Ala Trp
            180                 185                 190

Arg Glu Glu Pro Trp Ile His His Ala Pro Gln Gly Cys Gly Asn Ser
        195                 200                 205

Ser Arg Thr Ile Thr Gly Asp Thr Cys Asn Glu Glu Thr Gln Asn Leu
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Ser Thr Ile Tyr Leu Arg Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile
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225 230 235 240

Phe Ser Asp Tyr Gln Ser Glu Val Asp Ile Tyr Asn Arg Ile Arg Asp
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Glu Leu Met Asn Lys Val Lys Phe Tyr Val Leu Phe Thr Ala Leu Leu
260 265 270

Ser Ser Leu Cys Ala His Gly Ala Pro Gln Ser Ile Thr Glu Leu Cys
275 280 285

Ser Glu Tyr His Asn Thr Gln Ile Tyr Thr Ile Asn Asp Lys Ile Leu
290 295 300

Ser Tyr Thr Glu Ser Met Ala Gly Lys Arg Glu Met Val Ile Ile Thr
305 310 315 320

Phe Lys Ser Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln His
325 330 335

Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg
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Ile Thr Tyr Leu Thr Glu Thr Lys Ile Asp Lys Leu Cys Val Trp Asn
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Asn Lys Thr Pro Asn Ser Ile Ala Ala Ile Ser Met Glu Asn
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catttttttt attttattag catcgccatt atatgcaaat ggcgacagat tataccgtgc 240

tgactctaga cccccagatg aaataaaacg ttccggaggt cttatgccca gagggcataa 300

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gtattacaga aatctgaata tagctccggc agaggatggt tacagattag caggtttccc 720

accggatcac caagcttgga gagaagaacc ctggattcat catgcaccac aaggttgtgg 780

aaattcatca agaacaatca caggtgatac ttgtaatgag gagacccaga atctgagcac 840

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acggaatcga tggcaggcaa aagagaaatg gttatcatta catttaagag cggcgcaaca 1140

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aaagcatgtc taatgctagg aacctatata acaactactg tacttatact aatgagcctt 1380

atgctgcatt tgaaaaggcg gtagaggatg caataccgat ccttaaactg taacactata 1440

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<213> Escherichia coli

<220>
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Met Lys Asn Ile Thr Phe Ile Phe Phe Ile Leu Leu Ala Ser Pro Leu
1 5 10 15

Tyr Ala Asn Gly Asp Arg Leu Tyr Arg Ala Asp Ser Arg Pro Pro Asp
20 25 30

Glu Ile Lys Arg Ser Gly Gly Leu Met Pro Arg Gly His Asn Glu Tyr
35 40 45

Phe Asp Arg Gly Thr Gln Met Asn Ile Asn Leu Tyr Asp His Ala Arg
50 55 60

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Gly Thr Gln Thr Gly Phe Val Arg Tyr Asp Asp Gly Tyr Val Ser Thr
65                  70                  75                  80

Ser Leu Ser Leu Arg Ser Ala His Leu Ala Gly Gln Ser Ile Leu Ser
                85                  90                  95

Gly Tyr Ser Thr Tyr Tyr Ile Tyr Val Ile Ala Thr Ala Pro Asn Met
            100                 105                 110

Phe Asn Val Asn Asp Val Leu Gly Val Tyr Ser Pro His Pro Tyr Gln
        115                 120                 125

Val Ser Ala Leu Gly Gly Ile Pro Tyr Ser Gln Ile Tyr Gly Trp Tyr
    130                 135                 140

Arg Val Asn Phe Gly Val Ile Asp Glu Arg Leu His Arg Asn Arg Glu
145                 150                 155                 160

Tyr Arg Asp Arg Tyr Tyr Arg Asn Leu Asn Ile Ala Pro Ala Glu Asp
                165                 170                 175

Gly Tyr Arg Leu Ala Gly Phe Pro Pro Asp His Gln Ala Trp Arg Glu
            180                 185                 190

Glu Pro Trp Ile His His Ala Pro Gln Gly Cys Gly Asn Ser Ser Arg
        195                 200                 205

Thr Ile Thr Gly Asp Thr Cys Asn Glu Glu Thr Gln Asn Leu Ser Thr
    210                 215                 220

Ile Tyr Leu Arg Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile Phe Ser
225                 230                 235                 240

Asp Tyr Gln Ser Glu Val Asp Ile Tyr Asn Arg Ile Arg Asp Glu Leu
                245                 250                 255

Met Asn Lys Val Lys Phe Tyr Val Leu Phe Thr Ala Leu Leu Ser Ser
            260                 265                 270

Leu Cys Ala His Gly Ala Pro Gln Ser Ile Thr Glu Leu Cys Ser Glu
        275                 280                 285

Tyr His Asn Thr Gln Ile Tyr Thr Ile Asn Asp Lys Ile Leu Ser Tyr
    290                 295                 300

Thr Glu Ser Met Ala Gly Lys Arg Glu Met Val Ile Ile Thr Phe Lys
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Ser Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp
                325                 330                 335

Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Thr
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Tyr Leu Thr Glu Thr Lys Ile Asp Lys Leu Cys Val Trp Asn Asn Lys
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Thr Pro Asn Ser Ile Ala Ala Ile Ser Met Glu Asn
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<212> DNA
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acaaaccggc tttgtcagat atgatgacgg atatgtttcc acttctctta gtttgagaag      420

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acggcgttac tatcctctct atgtgcacac ggagctcctc agtctattac agaactatgt     1020

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